Those Amazing Molecular Motors

January 1, 2007

By Dr. David Rogstad

In my undergraduate course in biology at Caltech in the late 1950s, a cell was understood simply as a variety of chemical reactions going on inside a tiny test tube.1 Now, 50 years later, scientists know that the structure inside a cell is far more complex and exhibits elegant organization suggestive of a Designer.

Among other things, the cell includes an astonishing array of molecular motors, some of which travel along thin filaments just a few molecules in diameter. The cargoes needed for the various cell processes are hauled around the cell on these microfilaments, in a manner resembling the huge transportation systems found in a modern city.

Biologists have identified multiple categories of motor-proteins in the cell. Three that have been studied extensively are myosins, kinesins, and dyneins.2 The first two contain as many as 20 different classes, and in time it is likely many more will be discovered. The different categories reflect properties such as (a) the motors' exact shapes dictated by the proteins from which they are made; (b) the types of tracks the motors travel on, whether actin or microtubule microfilaments; and (c) the direction the motors travel along these microfilaments. Stunning illustrations of these motors (and other features and processes within the cell) can be seen in the 8-minute animated video *The Inner Life of a Cell*, available on Studio Daily.3

Researchers take special interest in comparing these biological motors with those designed by humans. Two key characteristics for comparison are efficiency (where 100% is maximum) and size. For man-made macroscopic devices, electric motors are the most efficient, operating at as much as 64% efficiency. For internal combustion engines, the efficiency rarely gets above 30%. No naturally occurring motors exist at this size.

However, when considering microscopic devices, scientists find many naturally occurring molecular motors that are incredibly small and highly efficient. Over the last few years, the emerging field of nanotechnology, which includes the study, design, and implementation of molecular-scale motors, has mimicked nature's elegance. While researchers can't yet build proteins with specific physical shapes, they have constructed motors relying on existing biological systems for components.

Research on the efficiency of nature's tiny motors is dazzling. The rotary motors of the bacterial cilia and flagellum demonstrate an efficiency near the perfect 100%.4 As a physicist familiar with the difficulty of designing and constructing small, efficient devices, I find this phenomenon absolutely remarkable.

Personal observations notwithstanding, scientists acknowledge that the motors found in biological systems are vastly superior to anything man-made. Nature's amazing molecular motors also show the characteristics that people usually associate with exquisite design *and* a Designer.

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Subjects: Biochemical Design

Dr. David Rogstad

Dr. Dave Rogstad received his PhD in physics from Caltech and worked over 30 years for NASA’s Jet Propulsion Laboratory. Though now retired, Dave continues to serve as an RTB board member and participates regularly in several RTB podcasts.

Little Motors, Big Designer

January 18, 2008

By Dr. David Rogstad

As a student I came across the humorous definition of a nuclear physicist as one who was “learning more and more about less and less, until finally he knew everything about nothing.” In today’s world of research, this reference to the wonders of nature at its tiniest levels could also be said about the biologist. Every day we are treated to new discoveries revealing the amazing intricacies of the biological cell and the molecular machines that govern its functionality, all at a size that requires an electron microscope to even begin to see.

In the middle of last year, *Science Magazine* published a fascinating [review article](http://www.sciencemag.org/cgi/content/full/317/5836/333) on the subject of molecular motors and their use in nanotechnology. In the first part of the article, the authors point out how the cell is best described as a miniature factory where literally thousands of machines perform various specialized tasks. These functions include: allowing the cell to replicate itself in under an hour (what factory do you know of that can perform this feat?), proofreading and repairing errors in its own manufacturing instructions (DNA), sensing its environment and responding to it, changing its shape and morphology, and obtaining energy from photosynthesis or metabolism.

To accomplish all of these tasks, the cell has a wide variety of specialized molecular motors that are direct analogs of the kind of devices that engineers design and build for man-sized factories. These include: “electric” motors having stators, rotors, shafts, bearings and universal joints; transport “trucks” that provide stepwise motion along “highways” called microtubules or filaments; and pumps made from tubes and cams that force fluids along the tubes. The major differences between these molecular motors and those made by humans are their size (a billion times smaller) and their efficiency (near 100 percent vs. 65 percent, at best).

If biomolecules can be successfully integrated into nanotechnology devices, there are several advantages, including the self-assembly characteristics of protein-based machines, the possibility of using other biological components from nature, and the fact that the processes for manufacture are environmentally benign and occur under mild conditions.

Research efforts in nanotechnology over the past several decades have produced various components of the machinery, like cogwheels or pumps, but have not yet been able to produce the motors needed to make the machinery go. The article asks whether the nano-machines found in nature can be used directly or serve as templates. So far, results indicate protein motors can be interfaced and made to drive the man-made nanoscale components but have limited lifetimes of only a few days. To date, no usable devices have been made. However, in the near future it is likely that progress will be made using the parts from cells, eventually allowing researchers to build tailor-made devices for the sorting of materials, assembly of different materials, concentration of materials for enhanced detection, along with many of the functions performed within cells.

One thing is clear: the machines found in cells are absolutely remarkable in their characteristics, challenging the minds and creativity of the most advanced researchers in nanotechnology. Yet, they are almost identical in form (but superior in efficiency and size) to the mechanical devices that the best engineers design for everyday life. Surely the biomachines found in cells require a level of intelligent design far greater than what man has accomplished!

Subjects: Biochemical Design, TCM - Biochemical Design

Dr. David Rogstad

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AAA+ Biomolecular Motors Provide A-1 Evidence for Design

October 29, 2009

By Dr. Fazale Rana

When I was a little kid, my dad used to insist I help him work on our family car. I'm sure he saw it as a way to teach me how automobiles operate and at the same time for us to bond; but I hated it.

We lived near West Virginia Institute of Technology in off-campus faculty housing. Our home was located on a hillside. A long set of stairs was the only way to reach our house from the street, which meant we didn't have a garage. Instead we parked the car next to the sidewalk, near the bottom of the stairs.

Every Saturday morning (or at least it seems to me like it was every Saturday), we worked on the car. To do this, we (and by "we," I mean I) had to carry tools from the house to the street. Invariably, we (and by "we," I mean my dad) needed a tool that we didn't have with us, which meant another trip up and down the stairs for me. My sojourn to retrieve the required tools would usually be repeated many times before my dad finished whatever he was doing with the car.

As much as I hated this ordeal, one of the things I did find fascinating, however, was how complex our car's engine was, and how my dad always seemed to know what part needed his attention. Even as a little kid, I knew just by looking under the hood that engineers—and pretty smart ones at that—were responsible for designing and assembling the engine.

One of the things I find intriguing as a biochemist is how much the inner workings of the cell have in common with an automobile engine. A number of protein complexes inside the cell operate as molecular-level machines. In fact, some of these machines bear a startling similarity to man-made machines. This similarity represents a potent argument for intelligent design.

I devoted an entire chapter to biomolecular motors in my book, [*The Cell's Design*](http://www.cellsdesign.com/) and have written articles on these fascinating protein systems. (Go [here](http://www.reasons.org/resources/publications/facts-faith/2000issue02#hume_vs_paley_these_motors_settle_the_debate), [here](http://www.reasons.org/articles/protein-structures-reveal-even-more-evidence-for-design), and [here](http://www.reasons.org/articles/increasing-the-torque-on-intelligent-design) to access a few of these pieces.)

[New work recently published](http://www.pnas.org/content/early/2009/10/13/0904756106.abstract) by a team from Japan identifies yet another protein complex with machine-like properties: the HslU transporter. This motor translocates protein chains into a large barrel-shaped conglomerate of proteins (called the bacterial energy-dependent proteolytic complex, HslUV for short) found in certain bacteria. HslUV degrades specific types of proteins and, consequently, plays a role in regulating the cell's activity.

[HslUV](http://mckaylab.stanford.edu/) consists of either one or two HslU motors that interact with the HslV complex. The HsLV ensemble is made up of twelve identical protein subunits arranged to form two rings (each ring is comprised of six subunits) stacked on each other. In this configuration, HslV forms a cylindrical structure with an internal cavity. Proteins are broken down within this cavity. HslU sits on top (or on the top and bottom if two HslU complexes are involved) of HslV, transporting protein chains into the HslV cavity.

Using a technique known as [molecular dynamics simulation](http://en.wikipedia.org/wiki/Molecular_dynamics), the research team explored the molecular-scale processes involved when the HslU motor moves protein chains into the HslV digestion chamber. Each HslU complex consists of a ring of six identical protein subunits. Located centrally within the ring is a pore.

The simulations indicated that the HslU motor transports extended protein chains through this pore via a paddling mechanism. The paddles are made up of two [tyrosine](http://en.wikipedia.org/wiki/File:L-tyrosine-3D-sticks.png)rings located across from each other within the interior of the pore. When provided with energy, the tyrosine rings/paddles move in a coordinated fashion, so that both rings circulate downward, away from each other, upward, and then toward each other.

When the tyrosine rings move toward each other they contact the protein chain; and as the rings move downward they drag the protein chain along. As the tyrosine paddles move away from each other, they disengage from the protein chain and re-engage it following their upward and inward movements. As this cycle repeats, the protein chain is transported in a step-wise manner into the HslV cavity as a result of the paddle-wheel motion.

The HslU motor is just one of a long list of molecular-level machines found inside the cell. The remarkable machine-like qualities of these biomolecular machines is provocative—even more so since [these systems operate with a greater degree of efficiency than man-made machines](http://www.reasons.org/articles/those-amazing-molecular-motors). They suggest that perhaps a mind is responsible for their creation; the same conclusion that even a small child would draw when peering under the hood of an automobile.

Subjects: Biochemical Design

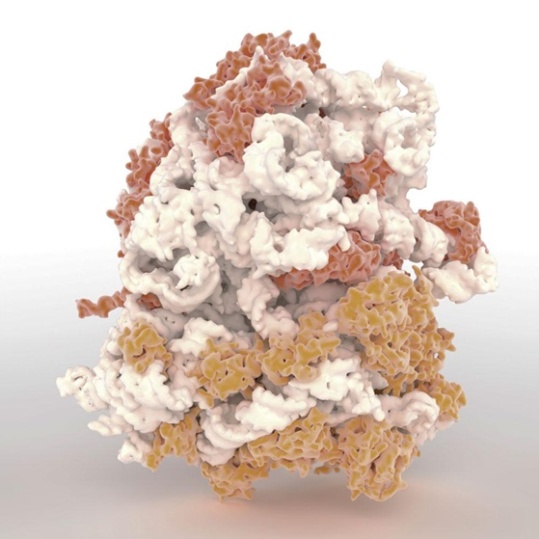
Dr. Fazale Rana

In 1999, I left my position in R&D at a Fortune 500 company to join Reasons to Believe because I felt the most important thing I could do as a scientist is to communicate to skeptics and believers alike the powerful scientific evidence—evidence that is being uncovered day after day—for God’s existence and the reliability of Scripture. [Read more about Dr. Fazale Rana](http://www.reasons.org/about/who-we-are/fazale-rana)



How the Central Dogma of Molecular Biology Points to Design

February 9, 2015

By Dr. Fazale Rana

From time to time, biochemists make discoveries that change the way we think about how life works. [In a recent paper](http://link.springer.com/article/10.1007/s11084-014-9354-9), Ian S. Dunn, a researcher at [CytoCure](http://www.cytocure.com/" \t "_blank), argues that biomolecules (such as [DNA](http://en.wikipedia.org/wiki/DNA), [RNA](http://en.wikipedia.org/wiki/RNA), and [proteins](http://en.wikipedia.org/wiki/Protein)) comprised of “molecular alphabets” (such as [nucleotides](http://en.wikipedia.org/wiki/Nucleotide) and [amino acids](http://en.wikipedia.org/wiki/Amino_acid)) are a universal requirement for life.1

Dunn’s work has far reaching implications. Perhaps the most significant relates to the [central dogma of molecular biology](http://en.wikipedia.org/wiki/Central_dogma_of_molecular_biology) (the organizing framework for biochemistry). First proposed by Francis Crick in 1956, the central dogma states that biochemical information flows from DNA through RNA to proteins.

The [RNA world hypothesis](http://en.wikipedia.org/wiki/RNA_world_hypothesis), a leading evolutionary explanation for life’s origin, supposes that the central dogma of molecular biology is an unintended outcome of chemical evolution. This hypothesis posits that initial biochemistry was built exclusively around RNA and only later did evolutionary processes transform the RNA world into the familiar DNA-protein world of contemporary organisms. Thus, the DNA-protein world is merely an accident, the contingent outcome of evolutionary history.

Origin-of-life researchers claimed support for the RNA world with the discovery of [ribozymes](http://en.wikipedia.org/wiki/Ribozyme) in the 1980s. These RNA molecules possess functional capabilities. In other words, RNA not only harbors information like DNA, it also carries out cellular functions like proteins. Researchers presumed that RNA biochemistry’s dual capabilities later apportioned between DNA (information storage) and proteins (function). Origin-of-life researchers often point to RNA’s intermediary role in the central dogma of molecular biology as further evidence for the RNA world hypothesis. In this view, RNA’s reduced role is a vestige of evolutionary history and RNA is viewed as a sort of molecular fossil.

However, if Dunn is correct and molecular alphabets are a universal requirement for life, it follows that the central dogma of molecular biology cannot be an accidental outcome of chemical evolution—a commonplace assumption on the part of many life scientists. Instead, it seems to be more appropriate to view this process as part of the Creator’s well-planned design.

**Chemical Complexity and Life**

Chemical complexity is a defining feature of life. In fact, the cellular operations fundamental to biology require chemical complexity. According to Dunn, this complexity can be achieved only through a large ensemble of macromolecules, each one carrying out a specific task in the cell. However, the [macromolecules](http://en.wikipedia.org/wiki/Macromolecule) must be assembled from molecular alphabets because only molecular alphabets allow for the plethora of combinatorial possibilities needed to give macromolecules the range of structural variability that makes possible the functional diversity required for life.

Proteins help illustrate Dunn’s point regarding combinatorial potential. Built from an alphabet that consists of 20 different amino acids, proteins are the workhorses of life. Each protein carries out a specific role in the cell. A typical protein might consist of 300 amino acids. So, for a protein of that size, the number of possible amino acid sequences is (20)300. Each sequence has the potential to form a distinct structure and, consequently, perform a distinct function. It is impossible to achieve this kind of complexity using small molecules or uniquely specified macromolecules.

**Two Types of Molecular Alphabets**

Another defining feature of life is its ability to replicate. For a cell to reproduce it must duplicate the information that specifies the functional macromolecules’ alphabet sequences and then pass it on to the daughter cells. Based on this requirement, Dunn identifies a need for primary and secondary molecular alphabets.

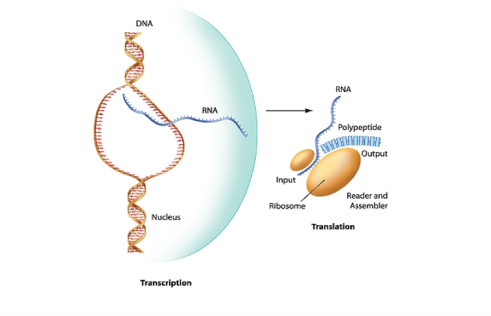
Macromolecules comprised of a primary molecular alphabet must be able to replicate themselves. This requirement, however, places constraints on the macromolecules, preventing them from being able to carry out the full range of functional activities needed to support the chemical complexity required for life. A secondary alphabet is needed to overcome this restriction. Specified by the primary alphabet, the secondary alphabet possesses the full range of functional possibilities because it is not constrained by the need to replicate.

DNA harbors the information a cell’s machinery needs to produce proteins and also possesses the ability to replicate. Therefore, DNA’s nucleotide sequence serves as a primary molecular alphabet while proteins’ amino acid sequences comprise a secondary molecular alphabet, enabling proteins to serve as the cell’s workhorse molecules.

**Molecular Alphabets and the Central Dogma of Molecular Biology**

According to the central dogma of molecular biology, the information stored in DNA is functionally expressed through the amino acid sequence and protein activity. When it is time for the cell’s machinery to produce a particular protein, it copies the appropriate information from the DNA alphabet and produces a molecule called [messenger RNA](http://en.wikipedia.org/wiki/Messenger_RNA) (mRNA). Once assembled, mRNA migrates to the [ribosome](http://en.wikipedia.org/wiki/Ribosome) and directs the synthesis of proteins.

In effect, the central dogma embodies the roles assumed by the primary and secondary molecular alphabets. Information in the cell’s primary molecular alphabet (DNA) is constrained by the need to replicate and so specifies the production of the cell’s secondary molecular alphabet (proteins) with the maximal amount of functional diversity. The translation from primary to secondary alphabet requires a decoding apparatus, which in the cell is comprised of RNA and ribosomes.



The key point is that the central dogma appears to be a fundamental requirement for life—a universal property, a necessary embodiment of life’s requisite chemical complexity. In this sense, it is reasonable to view the central dogma of molecular biology as part of the elegant, sophisticated, well-designed processes characteristic of biochemistry. Conversely, the central dogma of molecular biology can no longer be viewed as an accidental outcome of chemical evolution.

**Undermining the RNA World Hypothesis**

In the RNA world, the molecular alphabet that comprises RNA is a primary alphabet. But based on Dunn’s work, RNA would also have been constrained in its range of functional capabilities because of its need to replicate. Because of this restriction, the ribozymes of the RNA world cannot provide the chemical complexity necessary to sustain life. Dunn’s insight into the universal character of molecular alphabets unwittingly undercuts the RNA world scenario. Thus, it seems the central dogma of molecular biology (from DNA to RNA to proteins) had to be in place at the point that life originated.

Subjects: Biochemical Design

Dr. Fazale Rana

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Gene Architecture Illuminates the Brilliance of Life’s Molecular Logic

October 13, 2014

By Dr. Fazale Rana



Because of my responsibilities at Reasons to Believe, I spend a lot of time reading scientific magazines and journals. While I can make my way quickly through most of the articles, sometimes it takes me hours—even days—to read and process a single item published in a scientific journal, including those that are just a few pages long. And it’s not just the article length that determines my reading speed. The subject matter and organization of the piece make a difference, too.

Similar constraints confront the cell’s machinery when it reads, copies, and processes the information housed in [genes](http://en.wikipedia.org/wiki/Genes). The rate of [transcription](http://en.wikipedia.org/wiki/Transcription_(genetics))1 depends on gene length. Longer genes take more time to transcribe than shorter ones. But researchers from Portugal have just discovered that [genes’ content and organization also influence their transcription rate](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3989599/).2

This new insight provides researchers with a better understanding of how [gene expression](http://en.wikipedia.org/wiki/Gene_expression) occurs in the early stages of embryo development. It also highlights the elegant design and exquisite molecular logic of biological systems—a feature that reflects the work of a Mind.

**Researchers Study the Need for Rapid Gene Transcription**

The team from Portugal was studying the early stages of fruit fly embryonic development, at which point the embryonic cells divide rapidly (in a highly specialized form of cell division known as [syncytial nuclear division](http://en.wikipedia.org/wiki/Syncytium)). Rapidly dividing cells require the quick transcription of genes. If transcription does not happen fast enough, critical proteins won’t be available to support essential activities as the cell prepares to divide. As it turns out, during this stage of development, the most highly expressed genes tend to be smaller in size. They also lack [introns](http://en.wikipedia.org/wiki/Introns).

Introns are noncoding regions within genes. After messenger RNA is produced, the introns are excised and the remaining RNA fragments are spliced together. The [splicing process](http://en.wikipedia.org/wiki/Splicing_(genetics)) takes time—time that rapidly dividing cells don’t have.

The research team from Portugal discovered that 70 percent of the genes expressed during the early stages of embryonic development lack introns. Interestingly, only 20 percent of the genes, overall, in the fruit fly [genome](http://en.wikipedia.org/wiki/Genome) are intronless. So, clearly the size and structure of essential genes for the early stages of embryonic development have been optimized so they can be transcribed in a timely manner.

The researchers performed additional experiments to confirm this conclusion. In one study, they produced fruit flies with mutations to the genes for the cellular machinery that removes introns. They discovered that these mutations had no effect on the early stages of fruit fly embryogenesis (because most of the essential genes are intronless), but had devastating consequences later on in development when genes with introns are expressed at high levels.

They also incorporated a complex multi-intron gene into the fruit fly genome and rigged the gene so it would be expressed during the early stages of embryogenesis. The cells of the early-stage embryo couldn’t properly splice out the introns when this gene was transcribed.

The researchers think they have uncovered an important feature of early gene expression in embryogenesis. They also have exposed a relationship between gene structure and size and the rate of transcription that most likely applies to all rapidly dividing cells, not just those of fruit fly embryos.

**Elegant Gene Architecture Reflects a Creator’s Hand**

The optimization of gene size and architecture is just one more example of the superior molecular logic that undergirds biochemical systems. As a graduate student I recognized the elegance, sophistication, and cleverness of life’s chemical systems—and that realization played a role in convincing me a Creator must be responsible for life. (See “[Biochemistry and the Bible: Collaborators in Design](http://www.reasons.org/articles/biochemistry-and-the-bible-collaborators-in-design-an-interview-with-dr.-fuz-rana).”) Over the last three decades, as we’ve learned more about the structural design and operation of biochemical systems, the brilliance of life’s molecular logic shines even brighter. Because of this, I am more convinced than ever that life’s origin is the work of a Creator.

The Portugal research team attributes the optimal gene size and structure to evolutionary processes, which they believe shaped the genes over time for efficient transcription. Ironically, the team’s own experiments with genetically engineered and mutant embryos undermine their explanation.

For example, the experiments demonstrated that the early embryo’s rapidly dividing cells couldn’t effectively transcribe and process genes with several introns. If intron-laden genes happen to be essential for the early stage embryo, the embryonic cells won’t be able to divide, or at least, divide correctly, resulting in the death of the embryo. (A rule of thumb, disruptions to embryogenesis are much more catastrophic the earlier they occur in development.) Thus, the embryo will never develop into a reproductively mature individual, precluding evolutionary processes from shaping gene size and structure. To put it another way, the optimal gene size and architecture must be in place from the beginning for proper embryogenesis.

As we learn more and more about the structure and function of biochemical systems, the need to read between the lines lessens. The writing is on the wall: the elegant designs found throughout the biological realm evince the work of a Creator. It’s time to turn the page on the evolutionary paradigm.

Subjects: Biochemical Design

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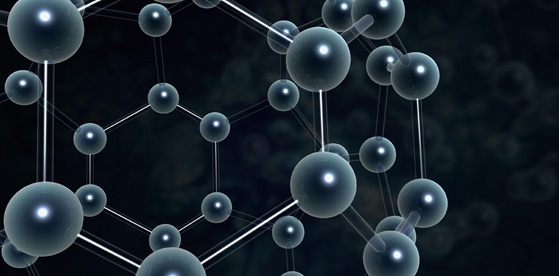
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Explanation for Origin-of-Life’s Molecular Handedness is Insoluble

May 8, 2008

By Dr. Fazale Rana



Another Mechanism to Explain Origin of Homochirality Questioned

One of my teenage daughters is left-handed. And nobody in our family wants to sit next to her when we eat at the table. It’s not because she has bad manners. It’s because her left arm bumps into the right arm of the person seated next to her. When it comes to meal time, left-handed and right-handed people don’t go well together.

The same is true for life. Left-handed and right-handed molecules don’t mix well. The building blocks of proteins (amino acids), DNA (deoxyribose), and RNA (ribose) have to be exclusively in left-handed (amino acids) and right-handed (deoxyribose and ribose) configurations—a condition called homochirality—for life’s chemistry to be possible.

Because of its central importance, origin-of-life investigators focus a lot of attention on trying to account for the origin of homochirality, so far without much success. (In fact, [I discussed this problem](http://www.reasons.org/articles/through-the-glass-darkly) a few weeks ago.) [New work\*](http://www.sciencedaily.com/releases/2008/04/080406114742.htm), however, has led a team of scientists to propose yet another mechanism to account for the genesis of homochirality. As with other proposals, this idea turns out to be unrealistic upon careful consideration.

To appreciate the discovery, I need to provide some background. For convenience, some of what follows is repeated from the earlier mentioned post on the origin of homochirality.

**Homochirality**

[Some molecules are mirror images of each other](http://en.wikipedia.org/wiki/Chirality_%28chemistry%29). Molecular mirror images result when four different chemical constituents bind to a central carbon atom. (The central carbon atom is called the chiral carbon.) These chemical groups are oriented in space in one of two possible arrangements that turn out to be reflections of each other. As mirror images, these compounds cannot be overlaid on one another so that all the chemical groups coincide in space. Because they can’t be superposed, molecular mirror images (called enantiomers) are distinct chemical entities.

Some of the compounds that play key roles as life’s building blocks, such as [amino acids](http://en.wikipedia.org/wiki/Amino_acid), and the sugars [deoxyribose](http://en.wikipedia.org/wiki/Deoxyribose) and [ribose](http://en.wikipedia.org/wiki/Ribose) are chiral compounds.

It turns out that the amino acids that comprise proteins and the sugars that are part of the constituents of DNA and RNA have uniform chirality, a condition biochemists call homochirality. In other words, all the amino acids in proteins have the same chirality. And all the sugars in DNA and RNA have identical chirality as well.

Homochirality is a strict requirement for life. Chirality dictates the three-dimensional positioning of chemical groups in space. And the spatial location of the chemical moieties (equal parts) plays an essential role in the interactions that stabilize the three-dimensional structure of proteins. (A protein’s structure determines its function.) As a case in point, for some proteins the incorporation of even one amino acid of the opposite mirror image into its backbone will disrupt the protein’s structure, and hence, function. Additionally, as Hugh Ross and I point out in [*Origins of Life*](http://www.reasons.org/catalog/origins-life)*,* laboratory experiments demonstrate that the “wrong” enantiomeric form of a [nucleotide](http://en.wikipedia.org/wiki/Nucleotide) inhibits the formation of DNA and RNA assembly.

**Homochirality and the Origin of Life**

In order to adequately explain the spontaneous emergence of life, origin-of-life researchers have to account for the origin of homochirality. This is no easy feat. While numerous proposed explanations for the genesis of homochirality have been advanced, none seem compelling and most are riddled with problems. (For a detailed discussion of some of the difficulties researchers encounter in their attempts to explain the origin of homochirality see [*Origins of Life*](http://www.reasons.org/catalog/origins-life).)

Part of this challenge stems from the fact that chemical reactions which generate chiral compounds from achiral starting materials produce a 50:50 mixture of both mirror images. (This type of mixture is called racemic.) In other words, chemical processes, as a rule of thumb, do not yield homochiral products—unless a chiral excess already exists at the outset for one of the reactants or the reaction catalyst.

**Does Crystallization Lead to Homochirality?**

A research team from Columbia University, headed up by [Ronald Breslow](http://www.columbia.edu/cu/chemistry/breslow/boss.html), believes it can explain how homochirality emerged. These investigators have [previously demonstrated](http://www.pnas.org/cgi/content/abstract/103/35/12979) that when amino acids crystallize out of solution in which there is a slight excess of one enantiomer, the ensuing crystal possesses a 50:50 mixture of the two enantiomers. On the other hand, the liquid phase becomes enriched with the enantiomer that initially was in slight excess. They have shown that a slight chiral excess of about 1% can quickly become amplified to about 90% after two rounds of crystallization. The reason for this enrichment stems from the reduced solubility of amino acid complexes formed when left-handed and right-handed versions combine compared to complexes formed from left-handed and left-handed forms (or right-handed and right-handed forms). The difference in solubility will cause the crystal to exclude the enantiomer that is initially in excess.

Based on this behavior, the Columbia team proposes the following scenario to explain how homochirality originated. First, they note that in meteorites like Murchison, [a slight chiral excess has been detected](http://www.reasons.org/articles/through-the-glass-darkly) for some amino acids recovered from the meteorite. Then they argue that meteorites delivering amino acids to early Earth would seed the oceans with a slight chiral excess of amino acids. As the oceans waters washed onto ancient shorelines and water evaporated, amino acid crystals would form, leaving behind an even greater chiral excess in the waters that returned to the oceans. Eventually, the amino acids in the oceans would be populated with nearly 100% of one enantiomer at the expense of the other. This end result, they claim, becomes the birth of homochirality as this chiral excess gets transferred to molecules taking part in the origin-of-life process.

At first glance this scenario seems quite reasonable. Closer examination, however, exposes a fundamental problem: chiral excess in Earth’s oceans will not promote homochirality in life molecules, but, in fact, detracts from it.

To illustrate, consider the reactions between amino acids to make peptides (small protein chains). Amino acids will not react with each other in water to form peptides. (In water the reverse reaction, in which peptides break down into the constitutive amino acids, is favored.) Origin-of-life researchers posit that this difficulty can be overcome if ocean waters deposit amino acids onto ancient shorelines. As the water evaporates, the reaction between amino acids becomes more likely. Additionally, the minerals on the shore can serve as catalysts promoting the reaction.

Herein lies the difficulty. According to the mechanism proposed by the Columbia chemists, the amino acids deposited on the shore will be a racemic mixture, displaying little if any chiral excess. The chirally enriched amino acids will be diluted out in the ocean waters and unable to react to form peptides.

In reality, the mechanism proposed by the Columbia scientists would inhibit the birth of homochirality, not promote it. Therefore, the homochirality problem still represents an “elbow-in-the-side” of chemical evolutionary explanations for the origin of life.

\*This study made science news headlines when first published. I discussed the scientific and biblical implications of this research on the [April 9, 2008 edition](http://www.podtrac.com/pts/redirect.mp3/c450913.r13.cf2.rackcdn.com/how-life-became-left-handed.mp3)of our new podcast, RTB’s *Science News Flash*. This podcast offers a unique Christian perspective on headline-grabbing discoveries. A free subscription to this podcast is available through iTunes.

Subjects: Panspermia, Prebiotic Chemistry, Primordial Soup

Dr. Fazale Rana

In 1999, I left my position in R&D at a Fortune 500 company to join Reasons to Believe because I felt the most important thing I could do as a scientist is to communicate to skeptics and believers alike the powerful scientific evidence—evidence that is being uncovered day after day—for God’s existence and the reliability of Scripture. [Read more about Dr. Fazale Rana](http://www.reasons.org/about/who-we-are/fazale-rana)



Failure of Molecular Clocks: Important Implications for the Christian Faith

July 1, 2000

By Dr. Fazale Rana

According to the biological evolutionary paradigm, molecular evolution parallels organic evolution. In other words, as the evolutionary changes proceed at the anatomical level (via the process of descent with modification from a common ancestor), molecular changes occur in the amino acid and nucleotide sequences of proteins and genes, respectively.1 These changes result from mutational events, the model says. Groups of organisms that have recently diverged from a common ancestor will have greater similarity in protein and gene sequences than groups of organisms that have diverged from the common ancestor in the more distant past.

If the mutational rate can be estimated and is approximately constant over time, then the time of divergence from the common ancestor can be determined from sequence differences. The mutational rate, or molecular clock, is estimated by comparing sequence differences for organisms with well-known times of origination (based on the fossil record).2 Once calibrated, the molecular clock can then be applied to estimate the time of origination for organisms with a poorly understood fossil record.

While straightforward in principle, application of molecular clock analysis is fraught with complications.3-4 For example, nuclear and mitochondrial genes mutate at different rates as do different genes/proteins within an organism. Moreover, the same gene/protein in different taxa (or groups) mutates at different rates.

Evolutionary biologists commonly use molecular clock analysis to estimate the timing of evolutionary events. Molecular clock analysis frequently yields results that disagree with the fossil record. One recent example that has implications for the biblical Creation Model is the dating of the origin of metazoons (complex animals). Based on the fossil record, essentially all animal phyla ever to exist throughout the earth’s history appeared suddenly and simultaneously within a narrow window of time (quite likely less than 3 million years) approximately 540 million years ago.5 This event, known as the Cambrian Explosion, creates a serious challenge to the evolutionary paradigm. In an attempt to escape the problem of the Cambrian Explosion, evolutionists have suggested that the Cambrian event is an artifact of an incomplete fossil record. To buttress this claim, evolutionary biologists have employed molecular clock analysis to argue that the divergence of animal phyla occurred as far back as 1.2 billion years ago.6 This would diffuse the explosive nature of the Cambrian event, giving the origin of animal phyla time to occur gradually over the course of 600 million years.

However, these molecular clock analyses have not gone uncontested.7 Recent work designed to evaluate the accuracy of the molecular clock technique, work done by two workers from the University of Illinois at Chicago (UI at C), decisively refutes the reliability of molecular clocks.8

In this study, the two biologists examined the accuracy of four molecular clocks operating within the order Perrisodactyla. This order includes the families Equidae (horses and zebras), tapiradae (tapirs), and Rhinoceritidae (rhinoceros). The Perrisodactyla fossil record is abundant and has well-defined origin dates. Based on the fossil record, the two researchers from UI at C defined two calibration points, at 3 million years ago and 50 million years ago, for two different genes yielding four molecular clocks. Unfortunately, all four molecular clocks produced disparate results, none of which agreed with the fossil record.

The failure of molecular clock analysis for such a cleanly-defined experimental system has two important implications for Christian apologetics:

1. **The molecular clock technique is not valid.** This means that the results challenging the completeness of the metazoon fossil record and the reality of the Cambrian Explosion are highly suspect. This helps preserve the Cambrian Explosion as a phenomenon that runs counter to naturalistic evolutionary models and is consistent with a Creation Model.
2. **At least one of the assumptions undergirding molecular clock analysis must be faulty**. The two assumptions are these: a) molecular clocks exist; and b) natural process evolution is a fact.  Evidence pointing to the latter continues to mount.

Subjects: Evolutionary Trees

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